

## SEQUENCE LISTING

5 <110> BASF Plant Science GmbH  
 SweTree Technologies AB

10 <120> POST HARVEST CONTROL OF GENETICALLY MODIFIED CROP GROWTH EM-  
 PLOYING D-AMINO ACID COMPOUNDS

15 <130> PF 55447 EP  
 <160> 16  
 <170> PatentIn version 3.1

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	Lys Arg Cys Thr Met Asp Ser Ser Asp Pro Ala Ser Pro Ala Tyr Ile	
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	Lys His Cys Leu Arg Leu Asp Pro Thr Ile Ser Ser Asp Gly Thr Ile	
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10 <213> Rhodosporidium toruloides

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40 Tyr Leu Ala Arg Glu Leu Gln Lys Leu Gly Ala Thr Phe Glu Arg Arg
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Glu Gly Ile Glu Val Leu Arg His Asn Val Gly Leu Arg Pro Ala Arg  
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Arg Thr Lys Ser Pro Leu Ser Leu Gly Arg Gly Ser Ala Arg Ala Ala  
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Thr Ile Pro Lys Glu His Ser Val Val Val Gly Ser Thr Lys Gln Asp  
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Thr Tyr Asp Val Gly Asn Trp Glu Ser Gln Pro Asp Pro Asn Ile Ala  
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15    <213>    *Trigonopsis variabilis*

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<213> *Trigonopsis variabilis*

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10	Arg	Glu	Leu	Trp	Glu	Tyr	Glu	Pro	Lys	His	Asp	Lys	Ile	Arg	Ser	Trp	
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	Asn	Thr	Tyr	Val	Arg	Asp	Phe	Lys	Val	Ile	Pro	Glu	Lys	Asp	Leu	Pro	
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	Pro	His	Tyr	Leu	Asn	Tyr	Met	Tyr	Lys	Leu	Leu	Ile	Glu	Ala	Gly	Val	
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	Glu	Cys	Val	Gly	Phe	Arg	Pro	Ser	Arg	Lys	Gly	Gly	Ala	Arg	Val	Glu	
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	Tyr Ile Ile Pro Arg Pro Leu Asn Gly Gly Val Ile Cys Gly Gly Phe				
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15	Met Gln Pro Gly Asn Trp Asp Arg Glu Ile His Pro Glu Asp Thr Leu				
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	Asp Ile Leu Lys Arg Thr Ser Ala Leu Met Pro Glu Leu Phe His Gly				
20	260		265		270
	Lys Gly Pro Glu Gly Ala Glu Ile Ile Gln Glu Cys Val Gly Phe Arg				
	275		280		285
	Pro Ser Arg Lys Gly Gly Ala Arg Val Glu Leu Asp Val Val Pro Gly				
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	Thr Ser Val Pro Leu Val His Asp Tyr Gly Ala Ser Gly Thr Gly Tyr				
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&lt;223&gt; DAAO signature

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	Gly Val Ile Gly Leu Thr Thr Ala Val Val Leu Ala Glu Arg Gly Arg	
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	cgg gtg cgg ctg tgg acc cgg gag ccc gcg gag cgg acc acc tcg gtg	150
	Arg Val Arg Leu Trp Thr Arg Glu Pro Ala Glu Arg Thr Thr Ser Val	
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15	Val Ala Gly Gly Leu Trp Trp Pro Tyr Arg Ile Glu Pro Val Ala Leu	
	45 50 55	
	gcc cag gcc tgg gcg ctg cgt tcc ctg gac gtg tac gag gag ctg gcg	246
	Ala Gln Ala Trp Ala Leu Arg Ser Leu Asp Val Tyr Glu Glu Leu Ala	
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	Ala Arg Pro Gly Gln Thr Gly Val Arg Met Leu Glu Gly Val Leu Gly	
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	Glu Thr Gly Leu Asp Glu Val Asp Gly Trp Ala Ala Ala Arg Leu Pro	
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	Gly Leu Arg Ala Ala Ser Ala Ala Glu Tyr Ala Gly Thr Gly Leu Trp	
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30	Ala Arg Leu Pro Leu Ile Asp Met Ser Thr His Leu Pro Trp Leu Arg	
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	Glu Arg Leu Leu Ala Ala Gly Gly Thr Val Glu Asp Arg Ala Val Thr	
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	Asp Leu Ala Glu Ala Asp Ala Pro Val Val Val Asn Cys Thr Gly Leu	
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	Gly Ala Arg Glu Leu Val Pro Asp Pro Ala Val Arg Pro Val Arg Gly	
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	cag ctg gtc gtc gtg gag aac ccc ggc atc cac aac tgg ctg gtc gcg	630
	Gln Leu Val Val Val Glu Asn Pro Gly Ile His Asn Trp Leu Val Ala	
	185 190 195 200	
	gcc gac gcg gac tcc ggg gag acg acg tac ttc ctt ccg cag ccg gga	678
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Arg Leu Leu Leu Gly Gly Thr Ala Glu Glu Asp Ala Trp Ser Thr Glu  
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 Tyr Arg Ile Glu Pro Val Ala Leu Ala Gln Ala Trp Ala Leu Arg Ser  
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 45 Arg Met Leu Glu Gly Val Leu Gly Glu Thr Gly Leu Asp Glu Val Asp  
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Gly Trp Ala Ala Ala Arg Leu Pro Gly Leu Arg Ala Ala Ser Ala Ala  
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5 Glu Tyr Ala Gly Thr Gly Leu Trp Ala Arg Leu Pro Leu Ile Asp Met  
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Ser Thr His Leu Pro Trp Leu Arg Glu Arg Leu Leu Ala Ala Gly Gly  
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10 Thr Val Glu Asp Arg Ala Val Thr Asp Leu Ala Glu Ala Asp Ala Pro  
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Thr Tyr Phe Leu Pro Gln Pro Gly Arg Leu Leu Leu Gly Gly Thr Ala  
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25 Glu Glu Asp Ala Trp Ser Thr Glu Pro Asp Pro Glu Val Ala Ala Ala  
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Ile Val Arg Arg Cys Ala Ala Leu Arg Pro Glu Ile Ala Gly Ala Arg  
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30 Val Leu Ala His Leu Val Gly Leu Arg Pro Ala Arg Asp Ala Val Arg  
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35 Leu Glu Arg Gly Thr Leu Pro Asp Gly Arg Arg Leu Val His Asn Tyr  
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10 act aca tac tgt tta atc tat gag gct gga tgt gct cca gct aaa att 96

Thr Thr Tyr Cys Leu Ile Tyr Glu Ala Gly Cys Ala Pro Ala Lys Ile

20 25 30

act att gtt gct gaa ttt tta cca ggt gat caa tct aca tta tat aca 144

Thr Ile Val Ala Glu Phe Leu Pro Gly Asp Gln Ser Thr Leu Tyr Thr

15 35 40 45

tct cca tgg gca ggt ggt aat ttt tct tgt att tca cca gct gat gat 192

Ser Pro Trp Ala Gly Gly Asn Phe Ser Cys Ile Ser Pro Ala Asp Asp

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acaaca ttg gct tat gat aaa ttc aca tat ctt aat tta ttc aag att 240

20 Thr Thr Leu Ala Tyr Asp Lys Phe Thr Tyr Leu Asn Leu Phe Lys Ile

65 70 75 80

cac aaa aaa tta ggt gga cca gaa tgt gga tta gat aat aag cca agt 288

His Lys Lys Leu Gly Gly Pro Glu Cys Gly Leu Asp Asn Lys Pro Ser

85 90 95

25 act gaa tat tgg gat ttt tat cct ggt gat gaa aaa gtc aat tct tta 336

Thr Glu Tyr Trp Asp Phe Tyr Pro Gly Asp Glu Lys Val Asn Ser Leu

100 105 110

aaa caa tat ctt aaa gat ttt aaa gtt att cca aaa tca gaa tta cca 384

Lys Gln Tyr Leu Lys Asp Phe Lys Val Ile Pro Lys Ser Glu Leu Pro

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gaa ggt gtt gaa tat ggt att agt tat act aca tgg aat ttc aac tgt 432

Glu Gly Val Glu Tyr Gly Ile Ser Tyr Thr Thr Trp Asn Phe Asn Cys

130 135 140

cct gtt ttc tta caa aat atg gct aat ttt tta aat aaa aga aat gtt 480

35 Pro Val Phe Leu Gln Asn Met Ala Asn Phe Leu Asn Lys Arg Asn Val

145 150 155 160

acc att att aga aaa cat tta aca cat att tct caa gct tat tta aca 528

Thr Ile Ile Arg Lys His Leu Thr His Ile Ser Gln Ala Tyr Leu Thr

165 170 175

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Val Asn Thr Lys Val Val Phe Asn Cys Thr Gly Ile Gly Ala Ala Asp

180 185 190

tta ggt ggt gtt aaa gat gaa aaa gtt tat cca act aga gga caa gtt 624

Leu Gly Gly Val Lys Asp Glu Lys Val Tyr Pro Thr Arg Gly Gln Val

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	ttt ggt ttt gaa act	gat gat att gtt agt	aga act aca tct tta tta	816
	Phe Gly Phe Glu Thr	Asp Asp Ile Val Ser	Arg Thr Thr Ser Leu Leu	
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	cca aag att tta gat	gaa cca ctt cat att	att aga gtt gca gct ggt	864
	Pro Lys Ile Leu Asp	Glu Pro Leu His Ile	Ile Arg Val Ala Ala Gly	
	275	280	285	
	tta aga cca agt aga	cat ggt ggt cca aga	att gaa gct gaa gtt tgt	912
15	Leu Arg Pro Ser Arg	His Gly Gly Pro Arg	Ile Glu Ala Glu Val Cys	
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	Glu Glu Gly Lys Leu	Thr Ile His Asn Tyr	Gly Ala Ser Gly Tyr Gly	
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20	tat caa gct ggt tat	ggt atg tct tat gaa	gct gtc aaa ctt tta gtt	1008
	Tyr Gln Ala Gly Tyr	Gly Met Ser Tyr Glu	Ala Val Lys Leu Leu Val	
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	Thr Ile Val Ala Glu	Phe Leu Pro Gly Asp	Gln Ser Thr Leu Tyr Thr	
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	Ser Pro Trp Ala Gly	Gly Asn Phe Ser Cys	Ile Ser Pro Ala Asp Asp	
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45	Thr Thr Leu Ala Tyr	Asp Lys Phe Thr Tyr	Leu Asn Leu Phe Lys Ile	
	65	70	75	80

	His	Lys	Lys	Leu	Gly	Gly	Pro	Glu	Cys	Gly	Leu	Asp	Asn	Lys	Pro	Ser	85	90	95
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	Lys	Gln	Tyr	Leu	Lys	Asp	Phe	Lys	Val	Ile	Pro	Lys	Ser	Glu	Leu	Pro	115	120	125
10	Glu	Gly	Val	Glu	Tyr	Gly	Ile	Ser	Tyr	Thr	Thr	Trp	Asn	Phe	Asn	Cys	130	135	140
	Pro	Val	Phe	Leu	Gln	Asn	Met	Ala	Asn	Phe	Leu	Asn	Lys	Arg	Asn	Val	145	150	155
15	Thr	Ile	Ile	Arg	Lys	His	Leu	Thr	His	Ile	Ser	Gln	Ala	Tyr	Leu	Thr	165	170	175
20	Val	Asn	Thr	Lys	Val	Val	Phe	Asn	Cys	Thr	Gly	Ile	Gly	Ala	Ala	Asp	180	185	190
	Leu	Gly	Gly	Val	Lys	Asp	Glu	Lys	Val	Tyr	Pro	Thr	Arg	Gly	Gln	Val	195	200	205
25	Val	Val	Val	Arg	Ala	Pro	His	Ile	Gln	Glu	Asn	Lys	Met	Arg	Trp	Gly	210	215	220
30	Lys	Asp	Tyr	Ala	Thr	Tyr	Ile	Ile	Pro	Arg	Pro	Tyr	Ser	Asn	Gly	Glu	225	230	235
	Leu	Val	Leu	Gly	Gly	Phe	Leu	Gln	Lys	Asp	Asn	Trp	Thr	Gly	Asn	Thr	245	250	255
35	Phe	Gly	Phe	Glu	Thr	Asp	Asp	Ile	Val	Ser	Arg	Thr	Thr	Ser	Leu	Leu	260	265	270
	Pro	Lys	Ile	Leu	Asp	Glu	Pro	Leu	His	Ile	Ile	Arg	Val	Ala	Ala	Gly	275	280	285
40	Leu	Arg	Pro	Ser	Arg	His	Gly	Gly	Pro	Arg	Ile	Glu	Ala	Glu	Val	Cys	290	295	300
45	Glu	Glu	Gly	Lys	Leu	Thr	Ile	His	Asn	Tyr	Gly	Ala	Ser	Gly	Tyr	Gly	305	310	315
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&lt;223&gt; Agrobacterium Left Border

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	ggactctaata	cataaaaaacc	catctcataa	ataacgtcat	gcattacatg	ttaattatta	540
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<223> complementary: coding for beta-glucuronidase (comprising intron)

<220>

15 <221> promoter

<222> (5148)..(6465)

<223> complementary: sTPT promoter

<220>

20 <221> misc\_feature

<222> (6537)..(6753)

<223> Agrobacterium Left Border

<400> 16

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